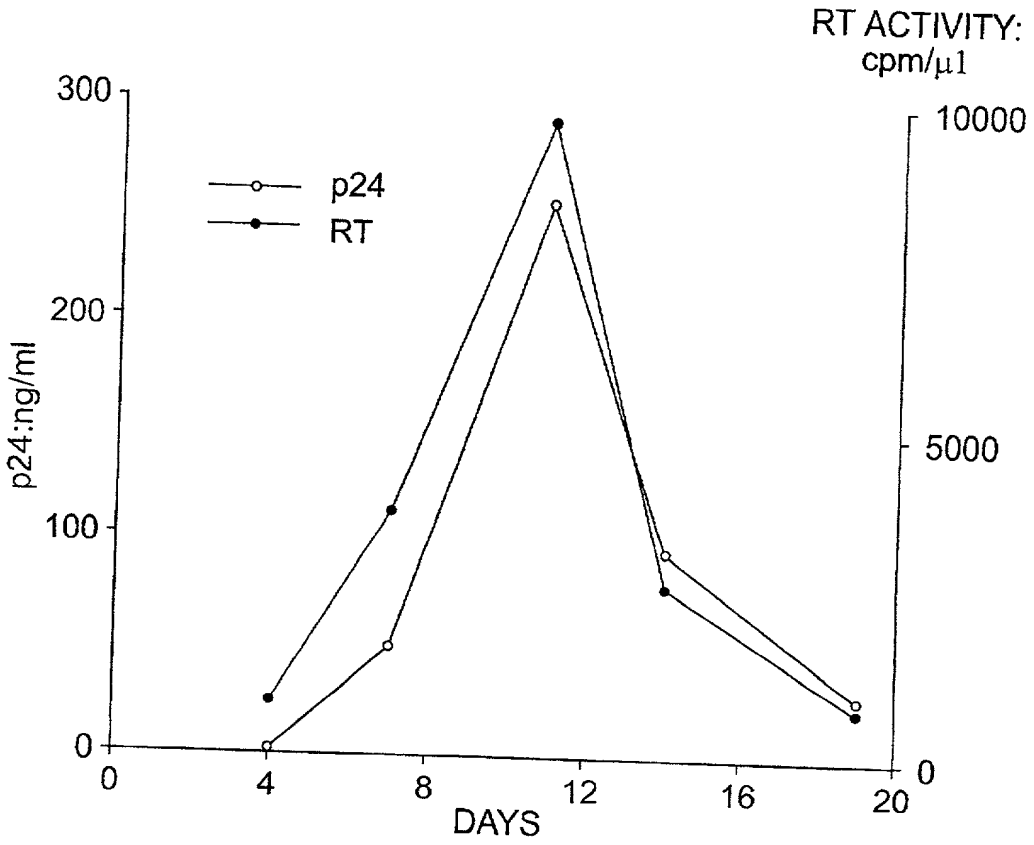

PRIMARY HIV-1 ISOLATE
RT ACTIVITY:
cpm/μl
10000
5000
0
300
200
100
0
p24:ng/ml
p24
RT
0
4
8
12
16
20
DAYS

FIG. 1A

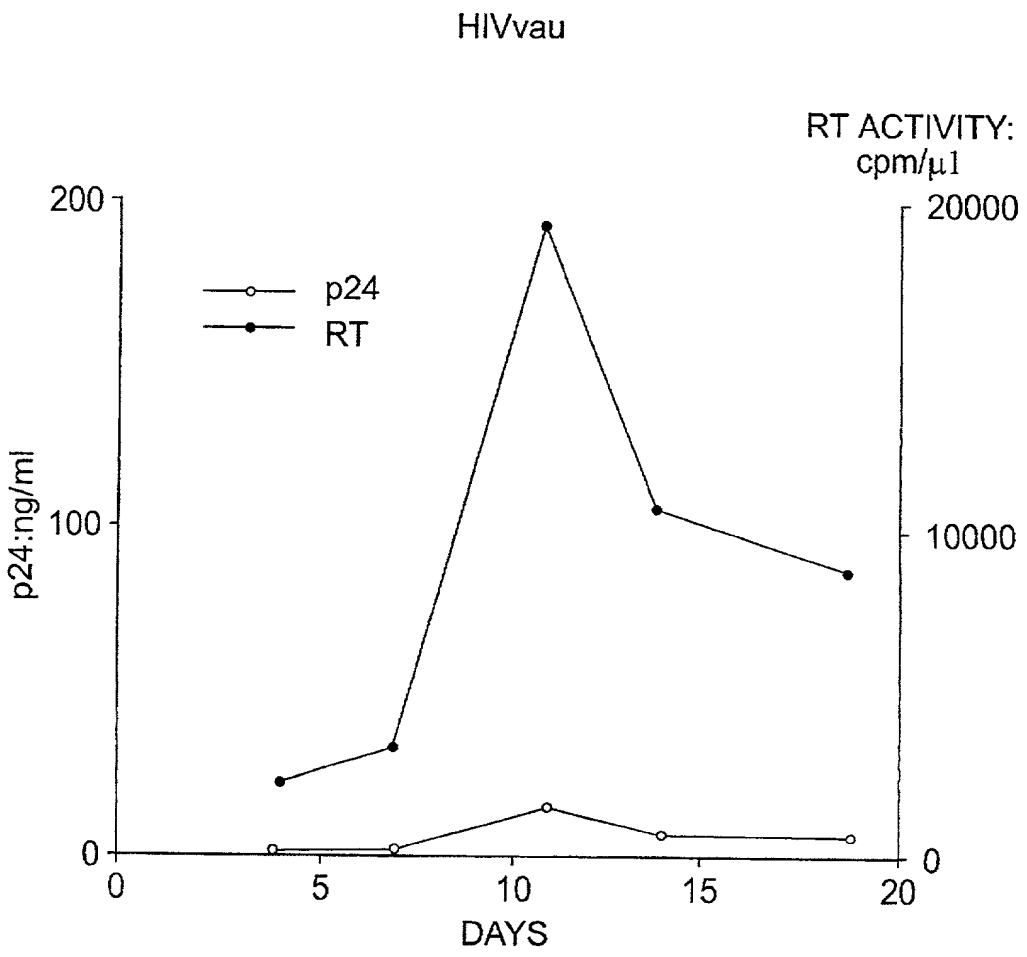

HIVvau
RT ACTIVITY:
cpm/µl
20000
10000
0
200
100
0
p24
RT
p24:ng/ml
0
5
10
15
20
DAYS

FIG. 1B

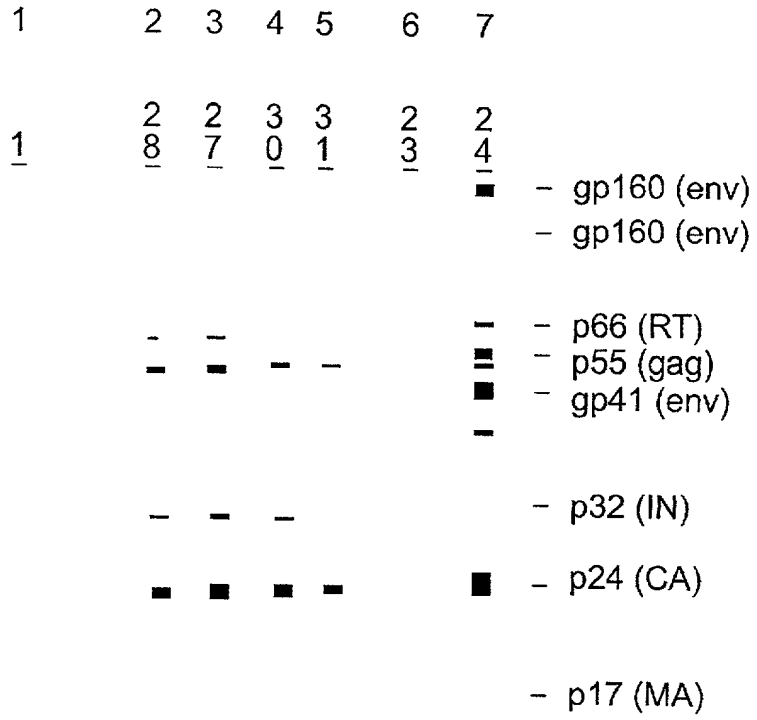

1
2
3
4
5
6
7
28
27
30
31
23
24
1
– gp160 (env)
– gp160 (env)
– p66 (RT)
– p55 (gag)
– gp41 (env)
– p32 (IN)
– p24 (CA)
– p17 (MA)

FIG. 2

```
                    SIGNAL PEPTIDE
                    .         .         .         .         .
VAU      1  ..MTAIMKAMGKRNRKLGIWCLILALIIPCLSCNQLYATVYSGVPVWEDA  48
            :..  . : ::.:|:|  .:::::::  | |..:.|:.||| |||||.:|
LAI      1  MRVKEKYQHLWRWGWKWG..TMLLGILMICSATEKLWVTVYYGVPVWKEA  48

                    .         .         .         .         .
VAU     49  KPTLFCASDANLTSTEQHNIWATQACVPTDPSPNEYELKNVTGKFNIWKN  98
            ..||||||||.  .|| ||:|||:|||||||.|.|  | |||:.||:|||
LAI     49  TTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKN  98

                    .         .         .         .         .
VAU     99  YIVDQMHEDIIDLWDQSLKPCVQMTFLCVQMNCTDIKNSINTTNSPLNSN  148
            :|:|||||||.||||||||||.:| ||| :.|||: |..||..|  ||.
LAI     99  DMVEQMHEDIISLWDQSLKPCVKLTPLCVSLKCTDLGNATNTNSSNTNSS  148

                    .         .         .         .         .
VAU    149  NTK......EVKQCDFNVTTVLKDKQEKKQALFYVTDLVKINATSNETMY  192
            ...      |:|.|.||:.| :::| :|. |:||  |::.|:  .:.| |
LAI    149  SGEMMMEKGEIKNCSFNISTSIRGKVQKEYAFFYKLDIIPID..NDTTSY  196
```

FIG. 3A

```
                   .         .         .         .         .
VAU  193  RLINCNSTTIRQACPKVSFEPIPIHYCAPAGCAIFKCNETGFNGTGLCKN  242
           |..||...| |||||||||||||||||||| ||:|||:..||||| |.|
LAI  193  TLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTN  246

                   .         .         .         .         .
VAU  243  VTVVTCTHGIKPTVSTQLILNGTLSKGNITIMGKNISDSGENILITLNTN  292
          |..| |||||:|.|||||:|||.|..:::.|.: |:.|.:..|:: || .
LAI  247  VSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS  296

                  V3 LOOP
                   .         .         .         .         .
VAU  293  ITIACERPGNQTIQKIMAGPMAWYSMALSNTKGDTRAAYCNYSATDWNKA  342
          :.|.|.||.|.| ..|. .. :  .:.  .. |: |.|.||.| ..|| .
LAI  297  VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWNAT  346

                   .         .         .         .         .
VAU  343  LKNITERYLELVEYNQTDVTMKFGNHSGEDAEVTNFFFNCHGEFFYCNTN  392
          ||.|..:. | .: |.| :   | . ||:|:|:..  ||| |||||||..
LAI  347  LKQIASKLREQFGNNKTII...FKQSSGGDPEIVTHSFNCGGEFFYCNST  393

                   .         .         .         .         .
VAU  393  RLFNHTFSCKKNMTNNKINCTNISNNSNGTQAI..PCRLRQVVRDWMRGG  440
          .||| |:        |.. :|: |||.:|.:.|  |||::|.:. |  .|
LAI  394  QLFNSTWF.......NSTWSTEGSNNTEGSDTITLPCRIKQFINMWQEVG  436
```

FIG. 3B

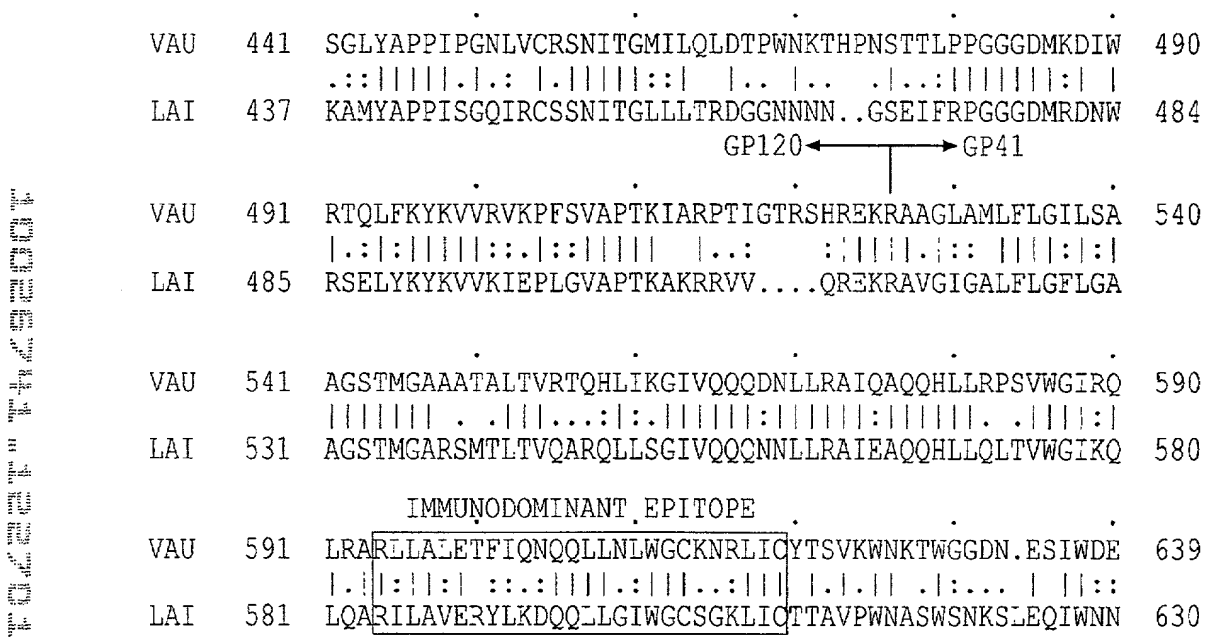

VAU 441 SGLYAPPIPGNLVCRSNITGMILQLDTPWNKTHPNSTTLPPGGGDMKDIW 490
LAI 437 KAMYAPPISGQIRCSSNITGLLLTRDGGNNNN..GSEIFRPGGGDMRDNW 484
GP120
GP41
VAU 491 RTQLFKYKVVRVKPFSVAPTKIARPTIGTRSHREKRAAGLAMLFLGILSA 540
LAI 485 RSELYKYKVVKIEPLGVAPTKAKRRVV....QREKRAVGIGALFLGFLGA
VAU 541 AGSTMGAAATALTVRTQHLIKGIVQQQDNLLRAIQAQQHLLRPSVWGIRQ 590
LAI 531 AGSTMGARSMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQ
IMMUNODOMINANT EPITOPE
VAU 591 LRARLLALETFIQNQQLLNLWGCKNRLICYTSVKWNKTWGGDN.ESIWDE 639
LAI 581 LQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNN 630

FIG. 3C

```
VAU   640  LTWQQWDQQINNVSSFIYEKIQEAQEQQEKNEKELLELDEWASIWNWLDI  689
LAI   631  MTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNI  680

VAU   690  TKWLWYIKIAIIIVGALIGVRVVMIVLNLVKNIRQGYQPLSLQIPIQQQA  739
LAI   681  TNWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPR  730

VAU   740  EVGTPGGTGEGGGDEDRRRWTPLPQGFLHLLYTDLRTIILWIYHLLSNLA  789
LAI   731  GPDRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRLRDLL  780

VAU   790  SEIQKLIRHLGLGLWIIGQRTIEACRLFKAIIQYWLQELQTSATNLLDTV  839
LAI   781  LIVTRIVE.......LLGRRGWEALKYWWNLLQYWSQELKNSAVSLLNAT  823

VAU   840  AVAVANWTDSTILGIQSIGRGILNIPRRIRQGLERLLL  877
LAI   824  AIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL  861
```

FIG. 3D

```
HIV-1lai        RILAVERYLKDQQLLGIWGCSGKLIC
HIV-1Z321       ------------------------I--
HIV-1eli        ------------------------H--
HIV-1JRCSF      -V-----------M-----------
HIV-1WMJ        -V-------R----------------
HIV-1NDK        -V-------R------------RH--
HIV-1mal        -V-------Q--R---M------H--
SIVCPZGAB       -L-------Q---I--L------AV-

vau             -L--L-TFIQN----NL---KNR---
mvp5180         -LQ-L-TLIQN--R-NL---K-----
ant70           -L--L-TL-QN----SL---K---V-

HIV-2rod        -VT-I-K--Q--AR-NS---AFRQV-
HIV-2D194       -VT-I-K-----AQ-NS---AFRQV-
```

FIG. 4

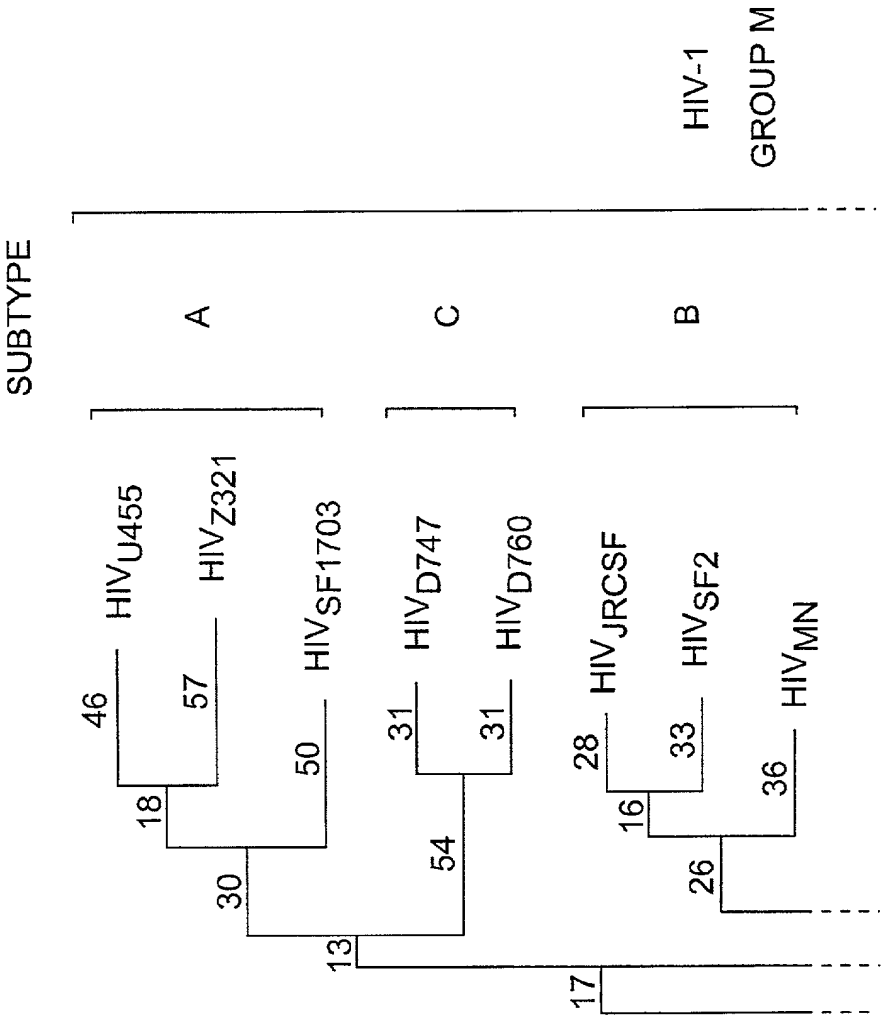

HIV-1
GROUP M
SUBTYPE
A
C
B
HIV$_{U455}$
HIV$_{Z321}$
HIV$_{SF1703}$
HIV$_{D747}$
HIV$_{D760}$
HIV$_{JRCSF}$
HIV$_{SF2}$
HIV$_{MN}$
46
57
50
31
31
28
33
36
18
54
16
30
26
13
17

FIG. 5A

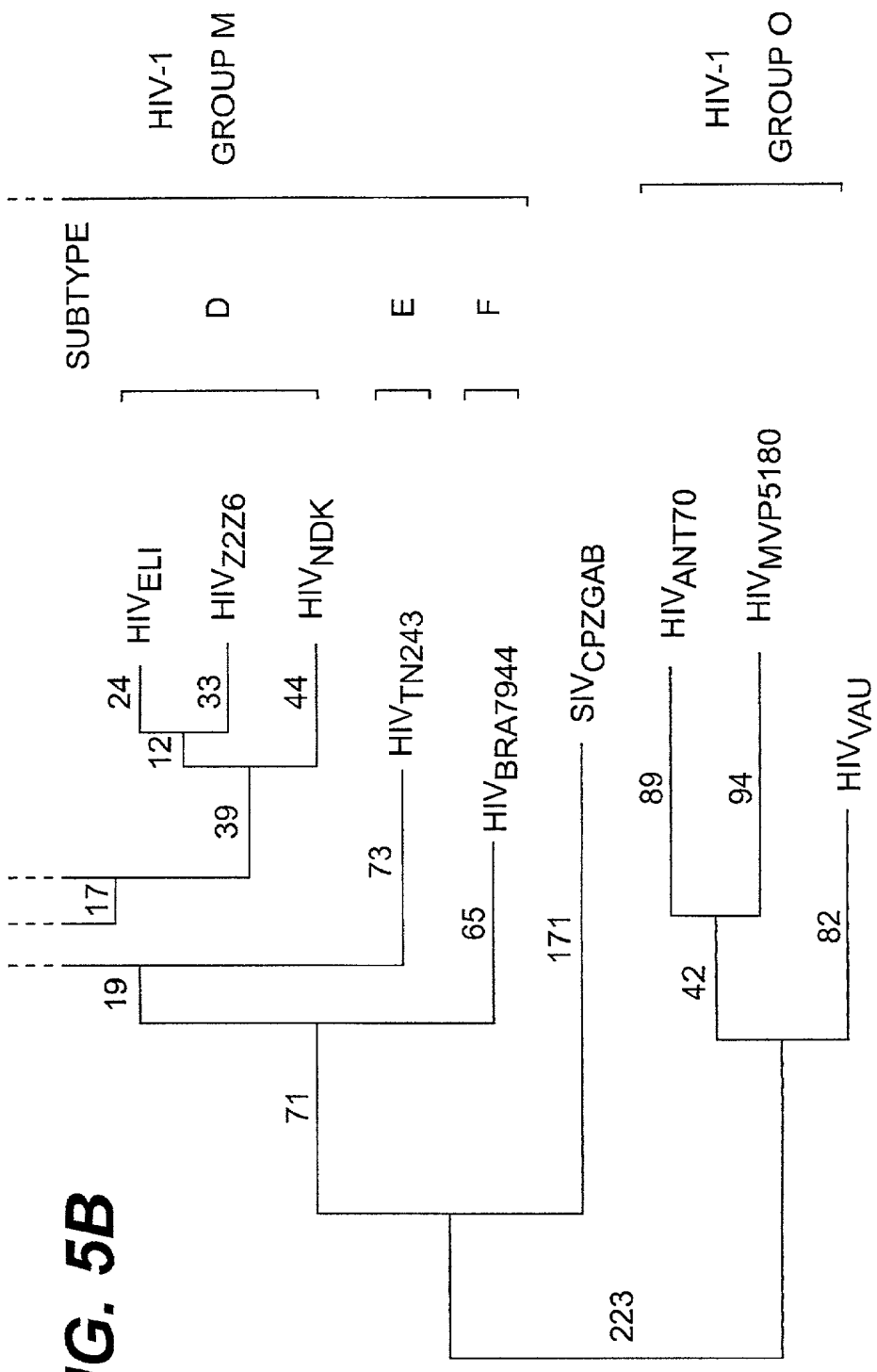

HIV-1
GROUP M
HIV-1
GROUP O
SUBTYPE
D
E
F
HIV$_{ELI}$
HIV$_{Z2Z6}$
HIV$_{NDK}$
HIV$_{TN243}$
HIV$_{BRA7944}$
SIV$_{CPZGAB}$
HIV$_{ANT70}$
HIV$_{MVP5180}$
HIV$_{VAU}$
24
33
44
12
39
17
73
65
19
71
171
89
94
42
82
223

FIG. 5B

DNA SEQUENCE 2631 B.P. ATGACAGCGATT ... CGACTCCTGTTA LINEAR

```
        |  10     |  20     |  30     |  40     |  50     |  60     |  70     |  80     |  90     | 100
   1 ATGACAGCGA TTATGAAAGC AATGGGGAAG AGGAACAGGA AGTTAGGGAT CTGGTGCTTG ATTTTGGCTT TGATAATCCC ATGTTTGAGC TGTAACCAAC
 101 TATATGCCAC AGTCTATTCT GGGGTACCTG TATGGGAAGA TGCAAAACCA ACATTGTTCT GTGCTTCAGA TGCTAACTTG ACAAGCACTG AACAGCATAA
 201 TATTTGGGCA ACACAAGCCT GTGTTCCCAC AGACCCCAGT CCAAATGAAT ATGAGCTAAA AAATGTGACA GGTAAATTCA ATATATGGAA AAATTATATA
 301 GTAGACCAAA TGCACGAAGA CATTATAGAT TTGTGGGACC AGAGTTTAAA ACCTTGTGTT CAAATGACTT TCTTGTGTGT ACAAATGAAT TGTACAGATA
 401 TCAAAAATAG TATTAATACC ACAAACAGTC CCTTAAACTC AAACAATACA AAAGAGGTGA AACAGTGTGA CTTTAATGTA ACTACAGTGC TCAAAGACAA
 501 ACAGGAGAAA AAACAGGCTC TATTCTATGT GACAGATTTG GTTAAGATTA ACGCCACATC AAATGAAACA ATGTATAGAT TAATTAATTG TAACTCCACA
 601 ACCATCAGGC AGGCCTGTCC AAAGGTATCT TTTGAGCCCA TTCCCATACA CTATTGTGCT CCAGCGGGAT GTGCCATCTT TAAGTGTAAT GAAACAGGAT
 701 TTAATGGAAC AGGTCTCTGT AAAAACGTTA CAGTAGTTAC TTGTACACAT GGCATCAAAC CAACAGTAAG TACCCAACTA ATACTAAATG GGACACTCTC
 801 TAAAGGAAAT ATAACAATCA TGGGAAAGAA TATTTCAGAC AGTGGGGAGA ACATCCTAAT AACCCTAAAT ACTAATATAA CAATAGCATG TGAGAGACCA
 901 GGAAATCAGA CAATACAAAA GATAATGGCA GGTCCAATGG CTTGGTACAG CATGGCCCTT AGTAATACAA AGGGGGATAC AAGGGCAGCT TATTGTAATT
1001 ATAGTGCCAC TGACTGGAAC AAAGCCTTAA AAAACATAAC TGAAAGATAT TTAGAACTTG TAGAATATAA TCAAACTGAT GTTACCATGA AATTCGGTAA
1101 TCACAGTGGT GAAGATGCAG AAGTAACAAA TTTCTTTTTT AACTGTCATG GAGAATTCTT TTATTGTAAC ACAAATCGGC TGTTTAATCA TACCTTTTCC
1201 TGCAAGAAGA ATATGACCAA TAACAAGATC AATTGTACTA ATATTAGCAA TAATAGCAAT GGCACTCAGG CAATACCTTG CAGGTTGAGA CAAGTAGTAA
1301 GGGACTGGAT GAGGGGAGGA TCGGGACTTT ATGCACCTCC CATCCCAGGA AACCTAGTAT GCAGGTCAAA CATAACTGGA ATGATTCTAC AATTGGACAC
1401 GCCATGGAAT AAAACACATC CTAACAGCAC CACCCTTAGA CCAGGAGGGG GAGATATGAA AGATATATGG AGAACTCAAT TGTTCAAATA TAAAGTAGTA
1501 AGAGTAAAAC CTTTTAGTGT AGCACCAACA AAAATTGCAA GGCCAACTAT AGGAACTAGA TCTCATAGAG AGAAAAGAGC AGCAGGTTTG GCAATGCTAT
1601 TCTTGGGGAT TCTAAGTGCA GCAGGAAGCA CTATGGGCGC AGCGGCAACA GCGCTGACGG TACGGACCCA GCATCTGATA AAGGGTATAG TGCAACAGCA
1701 GGATAACCTG CTAAGAGCAA TACAGGCCCA GCAACACTTG CTGAGGCCAT CTGTATGGGG TATTAGACAA CTCCGAGCTC GCCTGCTAGC CTTAGAAACC
1801 TTTATACAGA ATCAGCAACT CCTTAACCTG TGGGGCTGCA AGAATAGACT AATCTGCTAC ACATCAGTAA AGTGGAATAA AACATGGGGA GGAGATAATG
1901 AATCAATTTG GGATGAGTTA ACATGGCAGC AGTGGGATCA ACAGATAAAC AACGTAAGCT CCTTCATATA TGAAAAAATA CAAGAGGCAC AAGAACAACA
2001 GGAGAAAAAT GAGAAAGAAT TGCTGGAGTT AGATGAATGG GCCTCTATTT GGAATTGGCT TGACATAACT AAATGGTTGT GGTATATAAA AATAGCTATA
2101 ATCATAGTAG GAGCACTAAT AGGTGTAAGA GTAGTTATGA TAGTACTTAA TCTAGTAAAG AACATTAGGC AGGGATATCA ACCCCTCTCG TTACAGATCC
2201 CCATCCAACA ACAAGCGGAA GTAGGAACGC CAGGAGGAAC AGGAGAAGGA GGTGGAGACG AAGACAGGCG CAGGTGGACT CCATTGCCGC AAGGGTTCTT
2301 GCATCTGTTG TACACGGACC TCAGGACAAT AATCTTGTGG ATTTACCACC TCTTGAGCAA CTTAGCCTCA GAGATCCAGA AGTTGATCAG ACACCTGGGA
2401 CTTGGACTAT GGATCATAGG GCAGAGGACA ATTGAAGCTT GCAGACTCTT TAAAGCTATA ATACAATACT GGCTACAAGA ATTGCAAACT AGTGCTACAA
2501 ATCTACTAGA TACTGTTGCA GTGGCAGTTG CTAATTGGAC TGACAGCACA ATCTTAGGCA TACAAAGCAT AGGGAGAGGG ATTCTTAACA TACCAAGAAG
2601 GATTAGACAG GGCCTTGAAC GACTCCTGTT A
        |  10     |  20     |  30     |  40     |  50     |  60     |  70     |  80     |  90     | 100
```

FIG. 6

```
      |   10     |   20     |   30     |   40     |   50     |   60     |   70     |   80
  1 GCAGAGACAG GACAGGAAAC TGCCTACTTC CTGTTAAAAT TAGCAGCAAG ATGGCCTATT AAAATACTAC ATACAGACAA
 81 TGGGCCTAAC TTTACAAGTG CAGCCATGAA AGCTGCATGT TGGTGGACAA ACATACAACA TGAGTTTGGA ATACCATACA
161 ATCCACAAAG TCAAGGAGTA GTAGAAGCCA TGAACAAGGA ATTAAAATCA ATCATACAGG TGAGGGACCA AGCAGAGCAC
241 TTAAGGACAG CAGTACAAAT GGCAGTATTT GTTCACAATT TTAAAAGAAA AGGGGGGATT GGGGGGTACA CTGCAGGAGA
321 GAGATTAATA GACATATTAG CATCACAAAT ACAAACAACA GAACTACAAA AACAAATTTT AAAAATTCAA AATTTTCGGG
401 TCTATTACAG AGACAGCAGA GACCCTATTT GGAAAGGACC GGCACAGCTC CTG
      |   10     |   20     |   30     |   40     |   50     |   60     |   70     |   80
```

FIG. 7

GAG REGION

```
                        #      #  #    #        #        #      #

DUR  qgqmvhqalsprtlnawvkaveekafnpeiipmfmalsegavpydinvmlnaigghqgal
ANT  --------i--------------------------------is----t------------
MVP  --------i--------------------------------------t------------
LAI  --------i----------v------s--v----s------t-q-l-t---tv----a-m
MAL  ---i----i----------vi-----s--v----s------t-q-l-m---iv----a-m
CPZ  --------i----------v------s--v----s------l-q-v-t----v------m
```

FIG. 8A

```
                                  #   #    #   #          #    #

DUR     qvlkevindeaadwdrahpqqagplppgqireptgsdiagttstqqeqilwttragnpip
ANT     --------e--ve---t--ppv---------------------------h----pnq---
MVP     --------e---e---t--pam---------------------------i----gans--
LAI     -m---t--e---e---v--vh---ia---m---r----------l----g-m-nnp_---
MAL     -m--dt--e-------v--vh---i----m---r----------l----g-m-_snp---
CPZ     --------e---e---l--th---ia---l---r----------l----g---_-np---
                           |||                                  |||
```

FIG. 8B

```
                #  #        #

DUR     vgdiyrkwivlglnkmvkmyspvsildirqgpkepfrdyvdrfyktlrae
ANT     ----------------------------k---------------------
MVP     ------------------------------------------------
LAI     --e--kr--i-----i-r----t-------------------------
MAL     -----kr--i-----i-r-----------------------f------
CPZ     ---v--r-vi-----v-r--c---------------------------

HIV1-M / HIV1-O DISCRIMINATING POSITIONS  : #

HYPERVARIABLE REGIONS  :  ||||
```

FIG. 8C

REGION OF THE V3 LOOP OF GP120

```
----YK---QRTG-___---Q-LY-__THR-I-DI__-----        MAD
CTRPNNNTRKSIRIQRGPGRAFVT__IGK_IGNM__RQAHC        LAI
---------NR-S-_------H--__TKQ-I-DI__-----        OYI
-A--YQ---QRTP-__-L-QSLY-__TR_SRSII__G----        ELI
----G----RGIHF___---QALY-__T-_-V-DI__-R-Y-       MAL
-S--Y-TRKNIRRYSI-S-QAFYV__T---I-DI__-Q---        455
-H--G----GE__VQI---MTFYN__-ENVV-DT__-S-Y-        CPZ


-E--QI_DIQE__MRI--_M-WYSMG--GTA--S_S---Y-        ANT
-I-EGIAEVQD-YT___--_MRWRSM_TLIRSNNT_S-V-Y-       MVP
-E--G-QTIQK-MA___--_M-WYSMALSNTK-DT__-A-Y-       VAU
-V--G--SV-E-K-___--_M-WYSMQ-EREGKGANS-T-F-       DUR

C*R********I****GP_M*W*SM**********SR*A*C HIV-O CONSENSUS
CVRPGNNSVKEIKI__GP_MAWYSMQIEREGKGANSRTAFC        DUR
```

FIG. 9A

IMMUNODOMINANT REGION OF GP41

```
                    [~~~~~~~~~~~~~~~~~~~~~~]
                     [======================]

MAD          -V-------Q-------------H----T----S---
LAI          RILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWS
OYI          -V--------------------------T--------
ELI          ----------------------H----N----S---
MAL          -V-------Q--R---M------H----F----S---
455          -V-------Q------------------T----S---
CPZ          -L-------Q---I--L------AV-Y-T----N--P


ANT          -L--L-TL-QN----SL---K---V-Y-S-K--RT-I
MVP          -LQ-L-TLIQN--R-NL---K-----Y-S-K--RT-I
VAU          -L--L-TFIQN----NL---KNR---Y-S-K--KT-G
DUR          -L--L-TLMQN----NL---R--A--Y-S-Q--ET-G

HIV-O CONSENSUS  RL*ALET**QNQQ*L*LWGC*****CYTSV*WN*TW*

DUR          RLLALETLMQNQQLLNLWGCRGKAICYTSVQWNETWG
                          [_____________________]
                     [_____________________...
```

FIG. 9B

CAGGGACAAATGGTACATCAGGCCATCTCCCCCAGAACTTTATATGTATGGGTAAAGGCA
GTAGAAGAAAAGGCCTTTAACCCTGAAATTATCCCTATGTTTATGGCACTATCAGAAGGA
GCTGTTCCCTATGATATCAATGTTATGCTAAATGCCATAGGAGGACACCAAGGGGCTTTA
CAAGTATTAAAAGAAGTAATCAATGATGAAGCAGCAGACTGGGATAGAGCTCACCCACAA
CAGGCAGGGCCGTTACCACCAGGGCAGATAAGGGAACCAACAGGAAGTGACATTGCTGGA
ACAACTAGCACACAGCAAGAGCAAATTCTCTGGACTACTAGGGCAGGTAACCCTATCCCA
GTTGGAGACATCTATAGGAAATGGATAGTGTTGGGTCTAAACAAAATGGTAAAAATGTAT
AGTCCAGTGAGCATCTTAGATATTAGGCAGGGACCAAAAGAACCATTTAGAGATTATGTA
GACAGGTTCTACAAAACATTAAGAGCTGAGCAG

GAG REGION OF HIV1-O DUR STRAIN: 513 BASE PAIRS

= SEQ ID N° 9

QGQMVHQALSPRTLNAWVKAVEEKAFNPEIIPMFMALSEGAVPYDINVMLNAIGGHQGAL
QVLKEVINDEAADWDRAHPQQAGPLPPGQIREPTGSDIAGTTSTQQEQILWTTRAGNPIP
VGDIYRKWIVLGLNKMVKMYSPVSILDIRQGPKEPFRDYVDRFYKTLRAEQ

GAG REGION OF HIV1-O VIRUS DUR STRAIN: 171 AMINO ACIDS

FIG. 10

ATTCCAATACACTATTGTGCTCCAGCAGGATATGCTATCTTTAAATGCAACAACGAGGAG
TTTACTGGAAAAGGCCCATGTAACAACATTTCAGTAGTTACCTGTACACAGGGTATCAAG
CCAACAGTAAGCACTCATCTAATATTCAATGGGACAATCTCTGAAAGAAAAATAAGAATT
ATGGGAAAGAACATCTCGAGCAACTCAGGTAATATCCTAGTGACCCTAAATTCTACTATA
AACATGACCTGTGTGAGGCCAGGAAATAATTCAGTACAGGAGATAAAAATAGGTCCAATG
GCTTGGTACAGTATGCAAATTGAGCGAGAGGGAAAAGCAGCAAATTCAAGAACAGCTTTT
TGTACCTATAATGCCACGGACTGGAGAAAAACCTTGCAAGGGATAGCTGAAAGGTATTTA
GAACTTGTAAATAAAACAAGTCCGACTGAAATAATGTTCAATAAAAGCAATGGTGGAGAT
GCAGAAATAACCCGTTTGCATTTTAACTGTCATGGAGAATTCTTT

V3 LOOP OF GP120 DUR STRAIN: 525 BASE PAIRS

= SEQ ID N° 10

IPIHYCAPAGYAIFKCNNEEFTGKGPCNNISVVTCTQGIKPTVSTHLIFNGTISERKIRI
MGKNISSNSGNILVTLNSTINMTCVRPGNNSVQEIKIGPMAWYSMQIEREGKGANSRTAF
CTYNATDWRKTLQGIAERYLELVNKTSPTEIMFNKSNGGDAEITRLHFNSCGEFF

V3 LOOP OF GP120 DUR STRAIN: 175 AMINO ACIDS

FIG. 11

ATAGTGCAACAGCAGGACAACCTGCTGAGAGCAATACAGGCCCAGCAACATCTGCTGAGG
TTATCTGTATGGGGTATTAGACAACTCCGAGCTCGCCTGCTAGCCTTAGAAACCCTTATG
CAGAATCAGCAACTCCTAAACCTGTGGGGTTGTAGAGGAAAAGCAATCTGCTACACATCA
GTACAATGGAATGAAACATGGGGAGGAAATGACTCAATTTGGGACAGGTTAACATGGCAG
CAATGGGATCAACAGATAGCCAATGTAAGCTCTTTTATATATGACAAAATACAAGAAGCA
CAAGAACAACAA

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF HIV1-O DUR: 312 BASE PAIRS

= SEQ ID N° 11

IVQQQDNLLRAIQAQQHLLRLSVWGIRQLRARLLALETLMQNQQLLNLWGCRGKAICYTS
VQWNETWGGNDSIWDRLTWQQWDQQIANVSSFTYDKIQEAQEQQ

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF HIV1-O DUR - PREDICTED PROTEIN: 104 AMINO ACIDS

FIG. 12

SPECIFIC PRIMERS OF THE HIV-O TYPE

DUR V3a	ATT-CCA-ATA-CAC-TAT-TGT-GCT-CCA-3′
DUR V3r	AAA-GAA-TTC-TCC-ATG-ACT-GTT-AAA-3′
DUR 41a	GGT-ATA-GTG-CAA-CAG-CAG-GAC-AAC-3′
DUR 41r	AGA-GGC-CCA-TTC-ATC-TAA-CTC-3′

FIG. 13A

POSITIONS OF THE PRIMERS:

IN HIV MVP5180

dur V3a	6896 TO 6919
dur V3r	7400 TO 7423
dur 41a	7934 TO 7957
dur 41r	8292 TO 8302

IN HIV ANT70

dur V3a	6896 TO 6920
dur V3r	7392 TO 7415
dur 41a	7917 TO 7940
dur 41r	8256 TO 8276

IN HIV1 VAU

dur V3a	640 TO 663
dur V3r	1138 TO 1161
dur 41a	1684 TO 1707
dur 41r	2026 TO 2046

FIG. 13B

V3	
HIV1-M CONSENSUS	NEGATIVE
HIV1-M MAL (AFRICAN)	NEGATIVE
HIV1-M CTV-CPZ (CHIMPANZEE)	NEGATIVE
HIV1-O MVP5180	NEGATIVE
HIV1-O ANT70	POSITIVE

GP41	
HIV1-M CONSENSUS:	
-PASTEUR STANDARD	NEGATIVE
-INNOGENETICS RIGHT-EXTENDED	WEAK POSITIVE
HIV1-O MVP5180:	
-INNOGENETICS	NEGATIVE
-BEHRING LEFT-EXTENDED	POSITIVE
HIV1-O VAU	POSITIVE

FIG. 14

NUCLEOTIDE COMPARISONS

EXPRESSED AS PERCENTAGE DIFFERENCE

GP41 (OUT OF 330 BASES)

LAI	0						
MAL	11	0					
CPZ	33	31	0				
MVP5180	39	38	38	0			
ANT70	36	39	37	15	0		
VAU	39	38	38	14	14	0	
DUR	38	36	37	13	15	11	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	VAU	DUR

FIG. 15A

V3 (OUT OF 558 BASES)

LAI	0						
MAL	19	0					
CPZ	37	34	0				
MVP5180	46	43	45	0			
ANT70	45	44	43	23	0		
VAU	44	41	41	24	24	0	
DUR	46	43	42	25	22	24	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	VAU	DUR

GAG (OUT OF 520 BASES)

LAI	0					
MAL	9	0				
CPZ	21	25	0			
MVP5180	24	26	25	0		
ANT70	25	25	24	10	0	
DUR	25	26	25	9	10	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	DUR

FIG. 15B

PROTEIN COMPARISONS

EXPRESSED AS PERCENTAGE DIFFERENCE

GP41 (OUT OF 109 AMINO ACIDS)

LAI	0						
MAL	17	0					
CPZ	33	28	0				
MVP5180	42	40	41	0			
ANT70	42	45	39	22	0		
VAU	44	47	45	19	21	0	
DUR	44	42	39	17	17	14	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	VAU	DUR

FIG. 16A

V3 (OUT OF 186 AMINO ACIDS)

LAI	0						
MAL	31	0					
CPZ	46	39	0				
MVP5180	55	50	59	0			
ANT70	55	50	55	36	0		
VAU	55	51	55	39	36	0	
DUR	56	51	56	39	35	42	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	VAU	DUR

GAG (OUT OF 174 AMINO ACIDS)

LAI	0					
MAL	6	0				
CPZ	11	14	0			
MVP5180	21	23	18	0		
ANT70	21	24	19	6	0	
DUR	22	22	19	7	9	0
	LAI	MAL	CPZ	MVP 5180	ANT 70	DUR

FIG. 16B

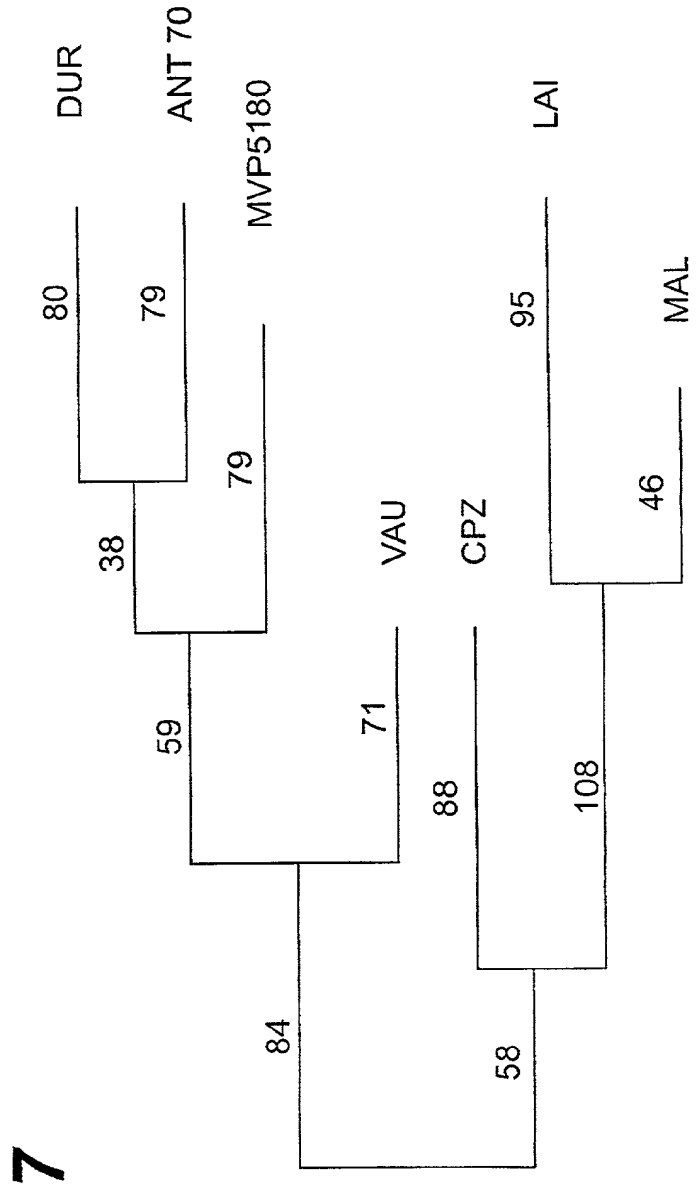
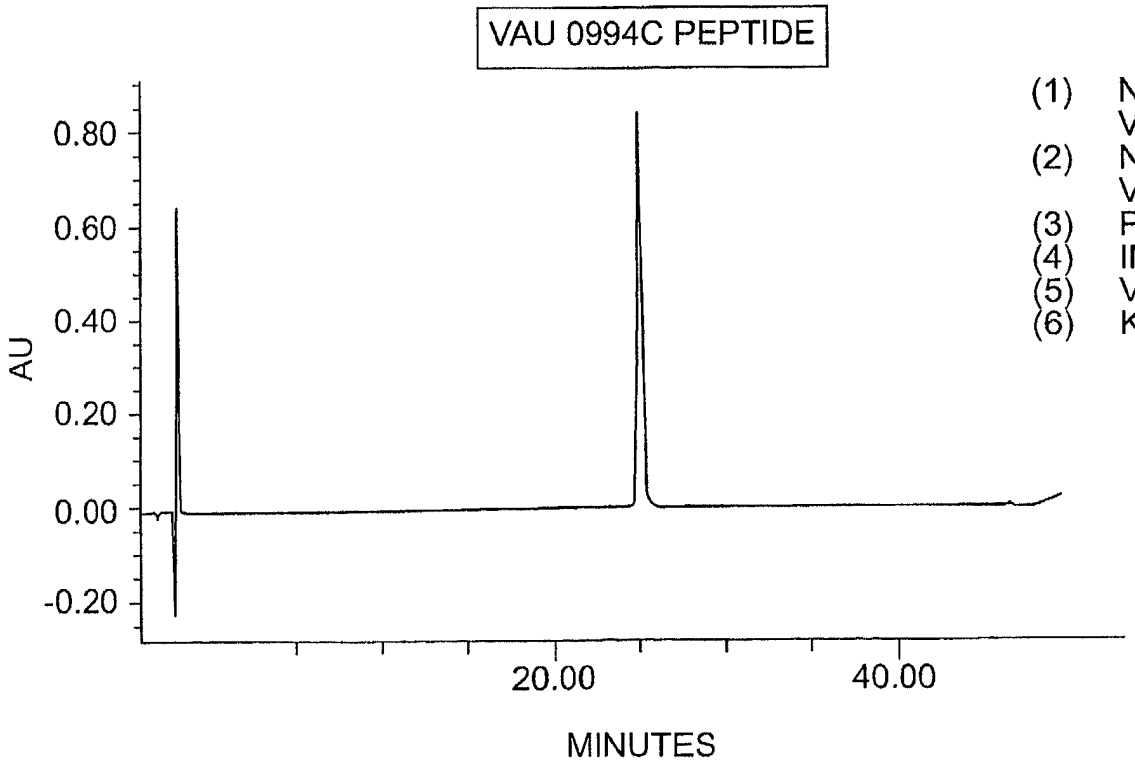


FIG. 17

PHYLOGENETIC TREE OF V3
(TREEALIGN PROGRAM, J. HEIN, ON BISANCE, CITI2)
(OUT OF 171 AMINO ACIDS)



(1) NAME OF THE SAMPLE: Vau7101550
(2) NAME OF THE METHOD: VauRepMel 3
(3) PROCESS: FvauPrcMel 3D
(4) INJECTION TIME: 45.0 MIN
(5) VOLUME: 50.00ml
(6) KIT: : MSHV15_5030mlml

FIG. 18A

CHROMATOGRAPHIC RESULTS

RETENTION TIME (MIN)	INITIAL TIME (MIN)	FINAL TIME (MIN)	% SURFACE AREA	INT TYPE
24.482	23.898	24.932	100.00	BB

FIG. 18B

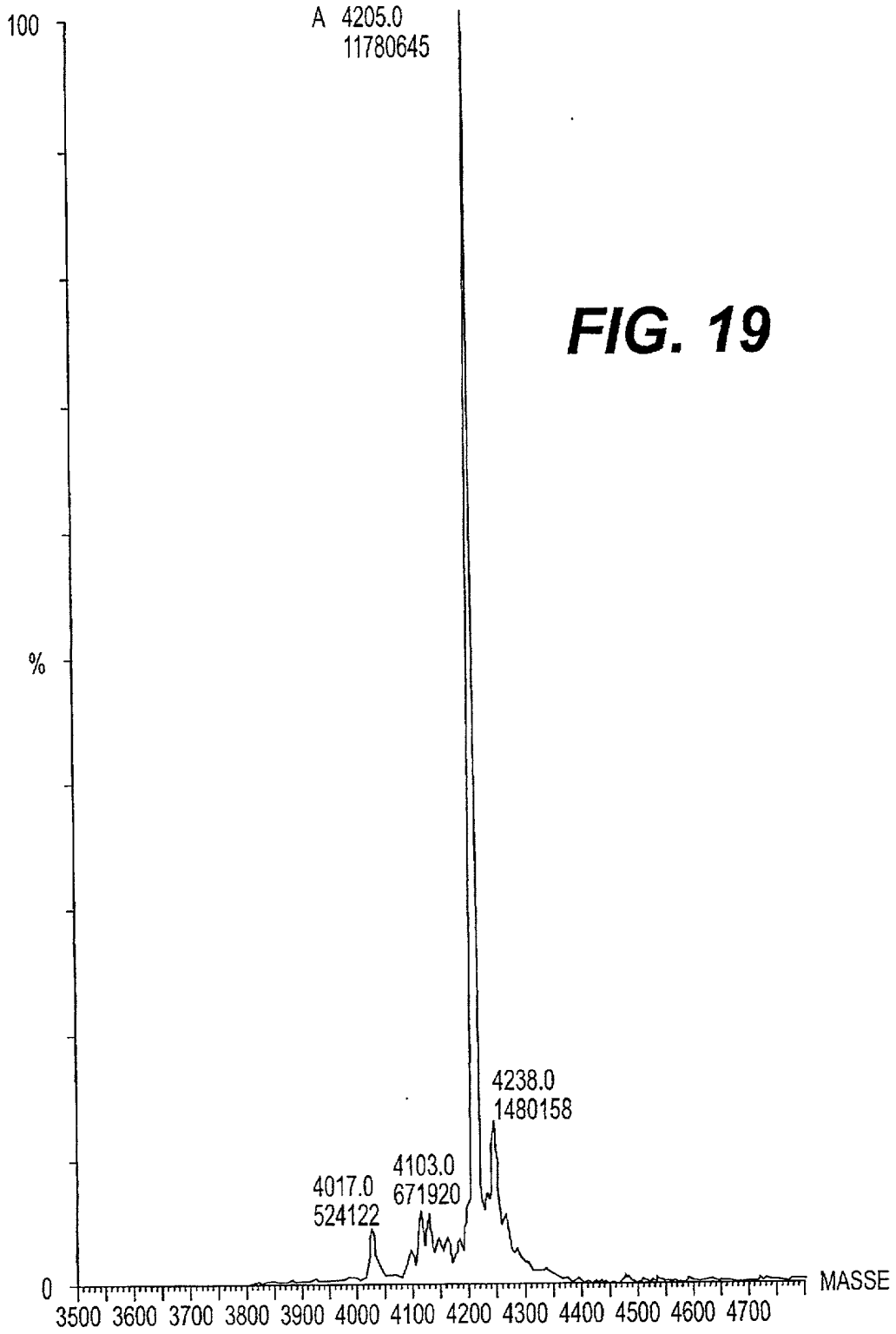

100
A 4205.0
11780645
%
4238.0
1480158
4103.0
671920
4017.0
524122
0
MASSE
3500 3600 3700 3800 3900 4000 4100 4200 4300 4400 4500 4600 4700

FIG. 19

VAU PEPTIDE

REF: F VAU 0994 C 710

SEQUENCE: RLLALETFIQNQQLLNLWGCKNRLICYTSVKWNKT

LENGTH: 35

MOLECULAR WEIGHT: 4210

ANALYTICAL CONTROLS: > 95% BY HPLC AND MASS SPECTROMETRY

FIG. 20

STUDY OF THE IMMUNOREACTIVITY OF THE PEPTIDE MIMICKING THE IMMUNODOMINANT EPITOPE OF THE GP160 VAU SEQUENCE (SUBTYPE O)

VS=0.1 RATIO	VAU PEPTIDE 2µg/ml
HIV1 SERA (PANEL BBI)	
BO1 NO° 12	0.80
BO1 NO° 13	0.40
BO1 NO° 15	0.80
PRB911K6	0.20
HIV1 SERA (ROMANIA) STAGE 3/4	
3989	9.50
5116	8.60
HIV1 SERA (PANEL AFM) SUBTYPE O	
MAA	>30
LOB	>30
HAM	>30
DUR	12.50
HIV1 SERUM (REIMS) SUB TYPE M?	
MAD	0.20

FIG. 21A

SUSPICION OF SUBTYPE O (YAOUNDE PASTEUR CENTER)	
	0.60
3372	>30
3361	28.80
1507	28.70
3167	>30
2628	28.10
1060	0.60
4020	0.30
4783	0.30
5322	0.40
6661	0.50
5527	0.30
5863	25.00
5969	>30
6487	>30
6509	0.70
6782	>30
5453	27.30
3826	1.50
HIV2 SERA	
BERT	0.30
PAOL	4.50
RIV	15.80

INDIRECT EIA PROCEDURE; 3 X 30 MIN TYPE GENELAVIA MIXT

NEGATIVE SERA	
N=48	
AVERAGE	0.022
DS	0.007
AVERAGE +12DS	0.107
VS	0.100

FIG. 21B

SUMMARY OF THE RESULTS OBTAINED ON THE AFRICAN SERA

	WB1 RESULTS									
	GP 160	GP 120	P 68	P 55	GP 41	P 40	P 34	P 25	P 18	
3361	++	+-	+				++	+	+	POS
1507	+	+-					+-	+-		POS
2628	+-		++	++		+	+	++	++	POS
3167	++	+	++	++	+	+	++	++	++	POS
3372	++	+-	+	++	+	+	++	++	+-	POS
5453	++	+-	+	+	+-	+	+	+	+	POS
5863	++	+-	+	+	+-	+-	+	+	+	POS
5969	+--		+	+		+	+	+		IND
6487	++		+	+			+	+-	+-	IND
6782	++		+	+	+	+	+	+		POS
950	+-		+-				+-	+-	+-	IND
1060	+-							+-	+	IND
5527										?
6509	++		+-				+--			IND
6661	+							+		IND
4020= SEMT	+							(+-)		IND
4783= 5322	+-							+-	+-	IND
3826								+-	+-	IND
MAD	++	+	+	+	+	+	+	+	+	POS
DUR										
MAA										
LOB	+		++	+-			++	++		IND
HAM			+				+	+		IND

=RATIO<1
=RATIO>2

FIG. 22A

	TEST DE SCREENING (RATIO : DO/VS)				
		GEM IND HIV1+2	ABBOTT SDW HIV1+2	MUREX SDW HIV1+2	
3361	0.10	18.00	0.56	0.72	1.40
1507	0.97	14.25	3.03	5.35	0.98
2628	0.70	18.00	4.84	1.71	1.34
3167	0.38	18.30	11.89	>6	0.88
3372	0.19	16.80	11.63	3.76	0.47
5453	2.50	>20			1.70
5863	2.30	>20			1.90
5969	2.30	15.20			2.25
6487	0.32	19.70			1.90
6782	0.07	13.40			2.95
950	1.20	6.00	5.76	>6	0.68
1060	0.60	18.00	0.46	1.25	0.67
5527	0.27	2.40			0.52
6509	0.32	>16			2.14
6661	8.10	10.10			1.54
4020= SEMT	0.23	6.30	1.03	4.98	4.12
4783= 5322	0.19	8.10 10.90	0.41		0.55 0.52
3826		3.93		1.64	0.72
MAD	-	+	+		
DUR		>8	2.00	0.80	
MAA					
LOB		>19	2.00	2.70	1.50
HAM		>19	1.80	7.80	2.70

FIG. 22B

	EIA PEPTIDES							
	CLONATEC RAP HIV1	39D6 HIV1B	FER HIV1B	39A HIV1B	VAU HIV1O	MVPP 5180 HIV1O	BNR 19 HIV1O	PEPTI-LAV1-2
3361	+				28.8	25.80	NT	
1507	DUBIOUS			8.4	28.7	28.80	1.7	
2628				3.6	28.1	19.30	1.2	
3167	+			>30	>30	>30	1.6	
3372	+-			2.8	>30	24.00	4.9	
5453	-	4.36	1.37	3.6	27.3		1.6	-
5863	-	1.42	0.40	1.4	25		0.5	-
5969	-	0.94	1.90	19.4	>30		0.6	+
6487	+	25.75	5.76	>30	>30		0.7	
6782	-	0.64	0.49	0.8	>30		10.3	-
950					0.6		0.4	
1060	DUBIOUS			1.9	0.6	0.40	0.6	
5527	-			4.5	0.3		0.2	+/-
6509	+			16.9	0.7		0.2	
6661	+			2.8	0.5		0.4	
4020= SEMT	?Ag-			1.15 1.2	0.3 0.7		0.5 0.9	
4783= 5322				2.5 4	0.3 0.4		0.3 0.3	
3826				1.6	1.5		0.7	
MAD		0.66	2.72	26.7	0.2		>30	-
DUR MAA LOB HAM		>30 1.02 0.73	>30 5.62 0.41	>30 NT 12.5 13.3	12.5 >30 >30 >30		0.2 NT >30 0.7	

FIG. 22C